

SEQUENCE LISTING



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<120> URATE OXIDASE

<130> 1579-379

<140> PCT/US99/17678

<141> 1999-08-05

<160>13

<170> PatentIn Ver. 2.0

<210> 1

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence:PBC CHIMERA

<400> 1

atg gct cat tac cgt aat gac tac aaa aag aat gat gag gta gag ttt	48
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe	
1 5 10 15	
gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag	96
Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	
20 25 30	
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480

Gln 145	Ile	Arg	Asn	Gly	Pro 150	Pro	Val	Ile	His	Ser 155	Gly	Ile	Lys	Asp	Leu 160	
aaa Lys	gtc Val	ttg Leu	aaa Lys	aca Thr	acc Thr	cag Gln	tct Ser	ggc Gly	ttt Phe	gaa Glu	gga Gly	ttc Phe	atc Ile	aag Lys	gac Asp	528
cag Gln	ttc Phe	acc Thr	acc Thr	ctc Leu	cct Pro	gag Glu	gtg Val	aag Lys	gac Asp	cgg Arg	tgc Cys	ttt Phe	gcc Ala	acc Thr	caa Gln	576
gtg Val	tac Tyr	tgc Cys	aaa Lys	tgg Trp	cgc Arg	tac Tyr	cac His	cag Gln	ggc Gly	aga Arg	gat Asp	gtg Val	gac Asp	ttt Phe	gag Glu	624
gcc Ala	acc Thr	tgg Trp	gac Asp	act Thr	gtt Val	agg Arg	agc Ser	att Ile	gtc Val	ctg Leu	cag Gln	aaa Lys	ttt Phe	gct Ala	ggg Gly	672
ccc Pro	tat Tyr	gac Asp	aaa Lys	ggc Gly	gag Glu	tac Tyr	tca Ser	ccc Pro	tct Ser	gtg Val	cag Gln	aag Lys	acc Thr	ctc Leu	tat Tyr	720
gat Asp	atc Ile	cag Gln	gtg Val	ctc Leu	tcc Ser	ctg Leu	agc Ser	cga Arg	gtt Val	cct Pro	gag Glu	ata Ile	gaa Glu	gat Asp	atg Met	768
gaa Glu	atc Ile	agc Ser	ctg Leu	cca Pro	aac Asn	att Ile	cac His	tac Tyr	ttc Phe	aat Asn	ata Ile	gac Asp	atg Met	tcc Ser	aaa Lys	816
atg Met	ggc Gly	ctg Leu	atc Ile	aac Asn	aag Lys	gaa Glu	gag Glu	gtc Val	ttg Leu	ctg Leu	cca Pro	tta Leu	gac Asp	aat Asn	cca Pro	864
tat Tyr	gga Gly	aaa Lys	att Ile	act Thr	ggc Gly	aca Thr	gtc Val	aag Lys	agg Arg	aag Lys	ttg Leu	tct Ser	tca Ser	aga Arg	ctg Leu	912
tga																915

<210> 2

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PBC CHIMERA

<400> 2

Met 1	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe 15
Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met 25	Ile	Lys	Val	Leu	His 30	Ile	Gln
Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln 45
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp 60
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys 80

Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu	
				85					90					95		
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val	
			100					105					110			
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	
		115					120					125				
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	
	130					135					140					
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
145					150					155					160	
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
			165						170					175		
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
			180					185					190			
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
		195					200					205				
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
	210					215					220					
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
225					230					235					240	
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
			245						250					255		
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
			260					265					270			
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
		275					280						285			
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
	290					295					300					

<210> 3

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence:pks chimera

<400> 3

atg	gct	cat	tac	cgt	aat	gac	tac	aaa	aag	aat	gat	gag	gta	gag	ttt	48
Met	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe	
1				5					10					15		

gtc	cga	act	ggc	tat	ggg	aag	gat	atg	ata	aaa	gtt	ctc	cat	att	cag	96
Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln	
			20					25					30			

cga	gat	gga	aaa	tat	cac	agc	att	aaa	gag	gtg	gca	act	tca	gtg	caa	144
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln		
		35					40					45					
ctg	act	ttg	agc	tcc	aaa	aaa	gat	tac	ctg	cat	gga	gac	aat	tca	gat	192	
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp		
	50					55					60						
gtc	atc	cct	aca	gac	acc	atc	aag	aac	aca	gtt	aat	gtc	ctg	gcg	aag	240	
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys		
	65				70					75					80		
ttc	aaa	ggc	atc	aaa	agc	ata	gaa	act	ttt	gct	gtg	act	atc	tgt	gag	288	
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu		
				85					90					95			
cat	ttc	ctt	tct	tcc	ttc	aag	cat	gtc	atc	aga	gct	caa	gtc	tat	gtg	336	
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val		
			100					105					110				
gaa	gaa	gtt	cct	tgg	aag	cgt	ttt	gaa	aag	aat	gga	gtt	aag	cat	gtc	384	
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val		
		115					120					125					
cat	gca	ttt	att	tat	act	cct	act	gga	acg	cac	ttc	tgt	gag	gtt	gaa	432	
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu		
	130					135					140						
cag	ata	agg	aat	gga	cct	cca	gtc	att	cat	tct	gga	atc	aaa	gac	cta	480	
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu		
	145				150					155					160		
aaa	gtc	ttg	aaa	aca	acc	cag	tct	ggc	ttt	gaa	gga	ttc	atc	aag	gac	528	
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp		
				165				170						175			
cag	ttc	acc	acc	ctc	cct	gag	gtg	aag	gac	cgg	tgc	ttt	gcc	acc	caa	576	
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln		
			180					185					190				
gtg	tac	tgc	aaa	tgg	cgc	tac	cac	cag	ggc	aga	gat	gtg	gac	ttt	gag	624	
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu		
		195					200					205					
gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672	
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly		
	210					215					220						
ccc	tat	gac	aaa	ggc	gag	tac	tcg	ccc	tct	gtc	cag	aag	aca	ctc	tat	720	
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr		
	225				230					235					240		
gac	atc	cag	gtg	ctc	acc	ctg	ggc	cag	gtt	cct	gag	ata	gaa	gat	atg	768	
Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met		
				245				250						255			
gaa	atc	agc	ctg	cca	aat	att	cac	tac	tta	aac	ata	gac	atg	tcc	aaa	816	
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Leu	Asn	Ile	Asp	Met	Ser	Lys		
			260					265					270				
atg	gga	ctg	atc	aac	aag	gaa	gag	gtc	ttg	cta	cct	tta	gac	aat	cca	864	
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro		
		275					280					285					
tat	gga	aaa	att	act	ggt	aca	gtc	aag	agg	aag	ttg	tct	tca	aga	ctg	912	
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu		
		290				295					300						

<210> 4
 <211> 304
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:pks chimera

<400> 4
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
 1 5 10 15
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro

275		280		285
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu				
290		295		300

<210> 5
 <211> 304
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:baboon D3H

<400> 5
 Met Ala His Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe
 1 5 10 15
 Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln
 20 25 30
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
 85 90 95
 Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295 300

<210> 6
<211> 304
<212> PRT
<213> baboon

<400> 6
Met Ala Asp Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe
1 5 10 15
Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln
20 25 30
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60
Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
65 70 75 80
Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
85 90 95
Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
100 105 110
Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
115 120 125
His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140
Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190
Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
195 200 205
Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
210 215 220
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240
Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
245 250 255
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295 300

<210> 7
<211> 304
<212> PRT
<213> pig

<400> 7
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
85 90 95

His Phe Leu Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys

260	265	270
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro		
275	280	285
Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu		
290	295	300

<210> 8
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PBC amino truncated

<400> 8
 Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly
 1 5 10 15
 Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
 20 25 30
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser
 225 230 235 240

Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	Glu	Ile	Ser	Leu	Pro	Asn
				245					250					255	
Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	Met	Gly	Leu	Ile	Asn	Lys
			260					265					270		
Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	Tyr	Gly	Lys	Ile	Thr	Gly
		275					280					285			
Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu						
	290					295									

<210> 9
 <211> 301
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PBC carboxy truncated

<400> 9															
Met	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe
1				5					10					15	
Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln
			20					25					30		
Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
		35					40					45			
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
	50					55					60				
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
	65				70					75					80
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu
				85					90					95	
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val
			100					105					110		
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val
		115					120					125			
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu
	130					135					140				
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu
	145				150					155					160
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp
				165					170					175	
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln
			180					185					190		
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu
		195					200					205			
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly
	210					215					220				

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
 260 265 270
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
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<210> 10

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PKS amino truncated

<400> 10

Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly
 1 5 10 15
 Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
 20 25 30
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr
 225 230 235 240
 Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
 245 250 255
 Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys
 260 265 270
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly
 275 280 285
 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295

<210> 11
 <211> 301
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PKS carboxy truncated

<400> 11
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
 1 5 10 15
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
290 295 300

<210> 12
<211> 915
<212> DNA
<213> PIG

<400> 12
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aaagagggtgg caacttcagt gcaactgact ttgagctcca aaaaagatta cctgcatgga 180
gacaattcag atgtcatccc tacagacacc atcaagaaca cagttaatgt cctggcgaag 240
ttcaaaggca tcaaaagcat agaaactttt gctgtgacta tctgtgagca ttctctttct 300
tccttcaagc atgtcatcag agctcaagtc tatgtggaag aagttccttg gaagcgtttt 360
gaaaagaatg gagttaagca tgtccatgca tttatttata ctccactagg aacgcacttc 420
tgtgaggttg aacagataag gaatggacct ccagtcattc attctggaat caaagaccta 480
aaagtcttga aaacaaccca gtctggcttt gaaggattca tcaaggacca gttcaccacc 540
ctccctgagg tgaaggaccg gtgctttgcc acccaagtgt actgcaaag ggcgtaccac 600
cagggcagag atgtggactt tgaggccacc tgggacactg ttaggagcat tgcctgcag 660
aaatttgctg ggccctatga caaaggcgag tactcgccct ctgtccagaa gacactctat 720
gacatccagg tgctcaccct gggccagggt cctgagatag aagatatgga aatcagcctg 780
ccaaatatc actacttaaa catagacatg tccaaaatgg gactgatcaa caaggaagag 840
gtcttgctac ctttagacaa tccatatggc aggattactg gtacagtcaa gaggaagctg 900
acttcaaggc tgtga 915

<210> 13
<211> 915
<212> DNA
<213> BABOON

<400> 13
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tatgggaagg atatggtaaa agttctccat attcagcgag atggaaaata tcacagcatt 120
aaagagggtgg caacttcagt gcaacttact ctgagttcca aaaaagatta cctgcatgga 180
gataattcag atatcatccc tacagacacc atcaagaaca cagttcatgt cttggcaaaag 240
tttaaggga tcaaaagcat agaagccttt ggtgtgaata tttgtgagta tttcttttct 300
tcttttaacc atgtaatccg agctcaagtc tacgtggaag aaatcccttg gaagcgctct 360
gaaaagaatg gagttaagca tgtccatgca tttattcaca ctcccactgg aacacacttc 420
tgtgaaagtga aacaactgag aagtggaccc cccgtcattc attctggaat caaagacctc 480
aaggtcttga aaacaacaca gtctggattt gaaggtttca tcaaggacca gttcaccacc 540
ctccctgagg tgaaggaccg atgctttgcc acccaagtgt actgcaagtg gcgctaccac 600
cagtgacagg atgtggactt cgaggctacc tggggcacca ttcgggacct tgcctggag 660
aaatttgctg ggccctatga caaaggcgag tactcaccct ctgtgcagaa gaccctctat 720
gatatccagg tgctctccct gagccgagtt cctgagatag aagatatgga aatcagcctg 780

ccaaacattc actacttcaa tatagacatg tccaaaatgg gtctgatcaa caaggaagag 840
gtcttgctgc cattagacaa tccatatgga aaaattactg gtacagtcaa gaggaagttg 900
tcttcaagac tgtga 915